

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/487,558

DATE: 11/23/2001

TIME: 14:45:29

Input Set : N:\Crf3\RULE60\09487558.raw

Output Set: N:\CRF3\11232001\I487558.raw

KFD
#14

11-26-01

ENTERED

1 <110> APPLICANT: Busby, Robert
 2 Cali, Brian
 3 Hecht, Peter
 4 Holtzman, Doug
 5 Madden, Kevin
 6 Maxon, Mary
 7 Milne, Todd
 8 Norman, Thea
 9 Royer, John
 10 Salama, Sofie
 11 Sherman, Amir
 12 Silva, Jeff
 13 Summers, Eric
 14 <120> TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production
 15 in Fungi
 16 <130> FILE REFERENCE: 109272.147
 17 <140> CURRENT APPLICATION NUMBER: 09/487,558
 18 <141> CURRENT FILING DATE: 2000-01-19
 19 <150> PRIOR APPLICATION NUMBER: US/09/801,368
 20 <151> PRIOR FILING DATE: 2001-03-07
 21 <150> PRIOR APPLICATION NUMBER: US 09/487,558
 22 <151> PRIOR FILING DATE: 2000-01-19
 23 <150> PRIOR APPLICATION NUMBER: US 60/160,587
 24 <151> PRIOR FILING DATE: 1999-10-20
 25 <160> NUMBER OF SEQ ID NOS: 440
 26 <170> SOFTWARE: PatentIn version 3.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 26
 30 <212> TYPE: DNA
 31 <213> ORGANISM: Aspergillus terreus
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 33 gaattcatgg aattcgttgc agaaaag 26
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 26
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Aspergillus terreus
 39 <400> SEQUENCE: 2
 40 ggatccttag aaatcttgaa agtatt 26
 42 <210> SEQ ID NO: 3
 43 <211> LENGTH: 34
 44 <212> TYPE: DNA
 45 <213> ORGANISM: Aspergillus nidulans
 46 <400> SEQUENCE: 3
 47 gcggccgcgg cgcccgccc atgtcaacaa gaat 34
 49 <210> SEQ ID NO: 4
 50 <211> LENGTH: 25
 51 <212> TYPE: DNA

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56 <210> SEQ ID NO: 5
57 <211> LENGTH: 30
58 <212> TYPE: DNA
59 <213> ORGANISM: Aspergillus nidulans
60 <400> SEQUENCE: 5
61      catggggccc cgtgatgtct acctgcccac                                30
63 <210> SEQ ID NO: 6
64 <211> LENGTH: 30
65 <212> TYPE: DNA
66 <213> ORGANISM: Aspergillus nidulans
67 <400> SEQUENCE: 6
68      catgatcgat tgtgggtagt taatggtatg                                30
70 <210> SEQ ID NO: 7
71 <211> LENGTH: 40
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: Oligonucleotide sequence used for PUMP1 PCR.
76 <400> SEQUENCE: 7
77      acaaaaaaagc aggctccaca atgacatccc accacgggtga                                40
79 <210> SEQ ID NO: 8
80 <211> LENGTH: 35
81 <212> TYPE: DNA
82 <213> ORGANISM: Artificial Sequence
83 <220> FEATURE:
84 <223> OTHER INFORMATION: Oligonucleotide sequence used for PUMP1 PCR.
85 <400> SEQUENCE: 8
86      acaagaaaagc tgggttcatt cgctccgtcc tttct                                35
88 <210> SEQ ID NO: 9
89 <211> LENGTH: 40
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: Oligonucleotide sequence used for PUMP2 PCR
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95      acaaaaaaagc aggctccaca atgggcccgcg gtgacactga                                40
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98 <211> LENGTH: 35
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
101 <220> FEATURE:
102 <223> OTHER INFORMATION: Oligonucleotide sequence for PUMP2 PCR.
103 <400> SEQUENCE: 10
104      acaagaaaagc tgggtctatt gggtaggcag gttga                                35
106 <210> SEQ ID NO: 11
107 <211> LENGTH: 29

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108 <212> TYPE: DNA
109 <213> ORGANISM: Saccharomyces cerevisiae
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114 <211> LENGTH: 29
115 <212> TYPE: DNA
116 <213> ORGANISM: Saccharomyces cerevisiae
117 <400> SEQUENCE: 12
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121 <211> LENGTH: 34
122 <212> TYPE: DNA
123 <213> ORGANISM: Aspergillus niger
124 <400> SEQUENCE: 13
125      catggggccc tctctccacc ggcactaaga tagc          34
127 <210> SEQ ID NO: 14
128 <211> LENGTH: 35
129 <212> TYPE: DNA
130 <213> ORGANISM: Aspergillus niger
131 <400> SEQUENCE: 14
132      cgcggtacca gcattggaaa aggagggggg ggaag          35
134 <210> SEQ ID NO: 15
135 <211> LENGTH: 34
136 <212> TYPE: DNA
137 <213> ORGANISM: Aspergillus nidulans
138 <400> SEQUENCE: 15
139      cgcggtacca tcacaacaag ttggtaacag tatc          34
141 <210> SEQ ID NO: 16
142 <211> LENGTH: 32
143 <212> TYPE: DNA
144 <213> ORGANISM: Aspergillus nidulans
145 <400> SEQUENCE: 16
146      ggactagtta acaagaçaca cttcttcttc tt            32
148 <210> SEQ ID NO: 17
149 <211> LENGTH: 33
150 <212> TYPE: DNA
151 <213> ORGANISM: Saccharomyces cerevisiae
152 <400> SEQUENCE: 17
153      cgcggtacct atcttcactc aatatacttc cta          33
155 <210> SEQ ID NO: 18
156 <211> LENGTH: 33
157 <212> TYPE: DNA
158 <213> ORGANISM: Saccharomyces cerevisiae
159 <400> SEQUENCE: 18
160      cccaagcttc atcggtgaaa cttgataacg cac          33
162 <210> SEQ ID NO: 19
163 <211> LENGTH: 33
164 <212> TYPE: DNA

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165 <213> ORGANISM: Aspergillus nidulans
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170 <211> LENGTH: 33
171 <212> TYPE: DNA
172 <213> ORGANISM: Aspergillus nidulans
173 <400> SEQUENCE: 20
174      ccgctcgagc tatagaatag tgcaagtgga agc                               33
176 <210> SEQ ID NO: 21
177 <211> LENGTH: 1629
178 <212> TYPE: DNA
179 <213> ORGANISM: Aspergillus terreus
180 <400> SEQUENCE: 21
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182      aatcatgtca ctggcctcag gctaggcctg gttgtgggtt cagtcactct ggtggcggtt      120
183      ctgatgctct tggatatgtc catcattgtc acggcgattc ctcacattac cgcccagttt      180
184      cattccctgg gcgatgtcgg atggtacgga agtgcgtatc ttctatcaag ctgtgccctc      240
185      caacccttgg caggcaaaact atacactctg ttgaccctga aatacacctt cctcgctttt      300
186      ctcggttgtt ttgagattgg atcggttctt tgcggcactg ctcgttcgtc aacctgtttg      360
187      attgtagggc gagcagtggc cggaatggga gggtcggggc tcaccaatgg cgcaatcacc      420
188      attctgtcgg cggcagctcc aaagcaacag caaccgctct tgattgggat catgatgggc      480
189      ctaagccaaa tcgccattgt atgtggaccg ttgcttgggg gtgctttcac gcagcacgca      540
190      agttggcggt ggtgttttta catcaacctt cccattgggg cgtttgccac atttctcctt      600
191      ctcgtcatcc agatcccca aagattgcca tccacgtcgg attcaaccac agacggcaca      660
192      aaccccaaga gaagaggggc tcgggacgtc ttgaccaaac tggatttcct tggattcgtg      720
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197      attttctcct actacctgcc tatctacttc caggcggtca agaattgttc tcccaccatg      1020
198      agtggagtgt atatgctgcc gggcatttgt ggacagatcg tcatggcgat tgtgacgggt      1080
199      gcaatcatcg gtaaaacagg ctattacgtt ccgtggggcg tcgcaagcgg gatccttgtg      1140
200      tccatatccg ccggacttgt atcgaccttc cagccggaaa cctcgattgc agcatgggtc      1200
201      atgtatcagt tcctgggagg cgtggggcga ggatgcggaa tgcaaaccct tgtcgtcgcc      1260
202      attcaaaatg cgctgcctcc acaaacgagc cccatcggca tttcgctagc catgttcggc      1320
203      cagacattcg gtggctcgct ttttctcacc ctgaccgaat tggtttttag caatggtttg      1380
204      gactctggtc tgcgccaata tgcgccaacc ctcaatgcac aggaggtaac agccgcaggg      1440
205      gccaccggtc tccgccaagt ggtccccgct cctctcatct ctcggtcctt cttagcatac      1500
206      agtaaaaggc tggaccatgc attctacgtt gcggtcggtg cgtctggagc taccttcac      1560
207      ttcgcctggg gtatggggccg gcttgcttgg agaggctggc ggatgcagga gaaaggacgg      1620
208      agcgaatga
210 <210> SEQ ID NO: 22
211 <211> LENGTH: 542
212 <212> TYPE: PRT
213 <213> ORGANISM: Aspergillus terreus
214 <400> SEQUENCE: 22
215      Met Thr Ser His His Gly Glu Thr Glu Lys Pro Gln Ser Asn Thr Ala
216      1              5              10              15

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217   Gln Met Gln Ile Asn His Val Thr Gly Leu Arg Leu Gly Leu Val Val
218               20                25                30
219   Val Ser Val Thr Leu Val Ala Phe Leu Met Leu Leu Asp Met Ser Ile
220               35                40                45
221   Ile Val Thr Ala Ile Pro His Ile Thr Ala Gln Phe His Ser Leu Gly
222               50                55                60
223   Asp Val Gly Trp Tyr Gly Ser Ala Tyr Leu Leu Ser Ser Cys Ala Leu
224               65                70                75                80
225   Gln Pro Leu Ala Gly Lys Leu Tyr Thr Leu Leu Thr Leu Lys Tyr Thr
226               85                90                95
227   Phe Leu Ala Phe Leu Gly Leu Phe Glu Ile Gly Ser Val Leu Cys Gly
228               100               105               110
229   Thr Ala Arg Ser Ser Thr Met Leu Ile Val Gly Arg Ala Val Ala Gly
230               115               120               125
231   Met Gly Gly Ser Gly Leu Thr Asn Gly Ala Ile Thr Ile Leu Ser Ala
232               130               135               140
233   Ala Ala Pro Lys Gln Gln Gln Pro Leu Leu Ile Gly Ile Met Met Gly
234               145               150               155               160
235   Leu Ser Gln Ile Ala Ile Val Cys Gly Pro Leu Leu Gly Gly Ala Phe
236               165               170               175
237   Thr Gln His Ala Ser Trp Arg Trp Cys Phe Tyr Ile Asn Leu Pro Ile
238               180               185               190
239   Gly Ala Phe Ala Thr Phe Leu Leu Leu Val Ile Gln Ile Pro Asn Arg
240               195               200               205
241   Leu Pro Ser Thr Ser Asp Ser Thr Thr Asp Gly Thr Asn Pro Lys Arg
242               210               215               220
243   Arg Gly Ala Arg Asp Val Leu Thr Gln Leu Asp Phe Leu Gly Phe Val
244               225               230               235               240
245   Leu Phe Ala Gly Phe Ala Ile Met Ile Ser Leu Ala Leu Glu Trp Gly
246               245               250               255
247   Gly Ser Asp Tyr Ala Trp Asn Ser Ser Val Ile Ile Gly Leu Phe Cys
248               260               265               270
249   Ala Ala Gly Val Ser Leu Val Leu Phe Gly Cys Trp Glu Arg His Val
250               275               280               285
251   Gly Gly Ala Val Ala Met Ile Pro Ile Ser Val Ala Ser Arg Arg Gln
252               290               295               300
253   Val Trp Cys Ser Cys Phe Phe Leu Gly Phe Phe Ser Gly Ala Leu Leu
254               305               310               315               320
255   Ile Phe Ser Tyr Tyr Leu Pro Ile Tyr Phe Gln Ala Val Lys Asn Val
256               325               330               335
257   Ser Pro Thr Met Ser Gly Val Tyr Met Leu Pro Gly Ile Gly Gly Gln
258               340               345               350
259   Ile Val Met Ala Ile Val Thr Gly Ala Ile Ile Gly Lys Thr Gly Tyr
260               355               360               365
261   Tyr Val Pro Trp Ala Leu Ala Ser Gly Ile Leu Val Ser Ile Ser Ala
262               370               375               380
263   Gly Leu Val Ser Thr Phe Gln Pro Glu Thr Ser Ile Ala Ala Trp Val
264               385               390               395               400
265   Met Tyr Gln Phe Leu Gly Gly Val Gly Arg Gly Cys Gly Met Gln Thr

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